

47



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/990,874

DATE: 05/22/2002

TIME: 12:21:03

Input Set : A:\PTO.DC.TXT

Output Set: N:\CRF3\05222002\I990874.raw

5 <110> APPLICANT: Sung, Wing
 8 <120> TITLE OF INVENTION: Xylanases with Enhanced Thermophilicity and Alkalophilicity
 11 <130> FILE REFERENCE: 07121.0003U1
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/990,874
 C--> 14 <141> CURRENT FILING DATE: 2002-04-30
 14 <160> NUMBER OF SEQ ID NOS: 54
 17 <170> SOFTWARE: PatentIn version 3.0
 21 <210> SEQ ID NO: 1
 23 <211> LENGTH: 184
 25 <212> TYPE: PRT
 27 <213> ORGANISM: Aspergillus niger
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 36 20 25 30
 38 Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly Ser
 39 35 40 45
 41 Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser Ser
 42 50 55 60
 44 Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gly Ala Glu Tyr
 45 65 70 75 80
 47 Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala Thr
 48 85 90 95
 50 Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys Thr
 51 100 105 110
 53 Asp Thr Arg Ile Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe Thr
 54 115 120 125
 59 Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val Thr
 60 130 135 140
 62 Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn Ser
 63 145 150 155 160
 65 Asp Phe Asn Tyr Gln Val Met Ala Val Glu Ala Trp Ser Gly Ala Gly
 66 165 170 175
 68 Ser Ala Ser Val Thr Ile Ser Ser
 69 180
 71 <210> SEQ ID NO: 2
 73 <211> LENGTH: 185
 75 <212> TYPE: PRT
 77 <213> ORGANISM: Aspergillus tubigensis
 81 <400> SEQUENCE: 2
 83 Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gln Asn Leu Gly Asp
 84 1 5 10 15

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86 Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu Asp
87      20      25      30
89 Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Gly Trp Thr Thr Gly
90      35      40      45
92 Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser
93      50      55      60
95 Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu
96 65      70      75      80
98 Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala
99      85      90      95
101 Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys
102      100      105      110
104 Thr Asp Thr Arg Ile Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe
105      115      120      125
107 Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val
108      130      135      140
110 Thr Val Ala Asn His Phe Asn Phe Trp Ala His His Gly Phe His Asn
111 145      150      155      160
113 Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala
114      165      170      175
117 Gly Ser Ala Ala Val Thr Ile Ser Ser
118      180      185
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124 <212> TYPE: PRT
126 <213> ORGANISM: Bacillus circulans
130 <400> SEQUENCE: 3
132 Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Ile Val
133 1      5      10      15
135 Asn Ala Val Asn Gly Ser Gly Gly Asn Tyr Ser Val Asn Trp Ser Asn
136      20      25      30
138 Thr Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Pro Phe
139      35      40      45
141 Arg Thr Ile Asn Tyr Asn Ala Gly Val Trp Ala Pro Asn Gly Asn Gly
142      50      55      60
144 Tyr Leu Thr Leu Tyr Gly Trp Thr Arg Ser Pro Leu Ile Glu Tyr Tyr
145 65      70      75      80
147 Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys Gly
148      85      90      95
150 Thr Val Lys Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Arg
151      100      105      110
153 Tyr Asn Ala Pro Ser Ile Asp Gly Asp Arg Thr Thr Phe Thr Gln Tyr
154      115      120      125
156 Trp Ser Val Arg Gln Ser Lys Arg Pro Thr Gly Ser Asn Ala Thr Ile
157      130      135      140
159 Thr Phe Thr Asn His Val Asn Ala Trp Lys Ser His Gly Met Asn Leu
160 145      150      155      160
162 Gly Ser Asn Trp Ala Tyr Gln Val Met Ala Thr Glu Gly Tyr Gln Ser
163      165      170      175

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165 Ser Gly Ser Ser Asn Val Thr Val Trp
166          180          185
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172 <212> TYPE: PRT
174 <213> ORGANISM: Bacillus pumilus
177 <400> SEQUENCE: 4
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182 Glu Leu Trp Lys Asp Tyr Gly Asn Thr Ser Met Thr Leu Asn Asn Gly
183          20          25          30
185 Gly Ala Phe Ser Ala Gly Trp Asn Asn Ile Gly Asn Ala Leu Phe Arg
186          35          40          45
188 Lys Gly Lys Lys Phe Asp Ser Thr Arg Thr His His Gln Leu Gly Asn
189          50          55          60
191 Ile Ser Ile Asn Tyr Asn Ala Ser Phe Asn Pro Ser Gly Asn Ser Tyr
192 65          70          75          80
194 Leu Cys Val Tyr Gly Trp Thr Gln Ser Pro Leu Ala Glu Tyr Tyr Ile
195          85          90          95
197 Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Ala Tyr Lys Gly Ser
198          100          105          110
200 Phe Tyr Ala Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Thr Arg Val
201          115          120          125
203 Asn Gln Pro Ser Ile Ile Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser
204          130          135          140
206 Val Arg Gln Thr Lys Arg Thr Ser Gly Thr Val Ser Val Ser Ala His
207 145          150          155          160
209 Phe Arg Lys Trp Glu Ser Leu Gly Met Pro Met Gly Lys Met Tyr Glu
210          165          170          175
212 Thr Ala Phe Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val
213          180          185          190
215 Met Thr Asn Gln Leu Phe Ile Gly Asn
216          195          200
218 <210> SEQ ID NO: 5
220 <211> LENGTH: 185
222 <212> TYPE: PRT
224 <213> ORGANISM: Bacillus subtilus
228 <400> SEQUENCE: 5
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232 1          5          10          15
234 Asn Ala Val Asn Gly Ser Gly Gly Asn Tyr Ser Val Asn Trp Ser Asn
235          20          25          30
237 Thr Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Pro Phe
238          35          40          45
240 Arg Thr Ile Asn Tyr Asn Ala Gly Val Trp Ala Pro Asn Gly Asn Gly
241          50          55          60
243 Tyr Leu Thr Leu Tyr Gly Trp Thr Arg Ser Pro Leu Ile Glu Tyr Tyr
244 65          70          75          80
246 Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys Gly

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247          85          90          95
249 Thr Val Lys Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr Arg
250          100          105          110
252 Tyr Asn Ala Pro Ser Ile Asp Gly Asp Arg Thr Thr Phe Thr Gln Tyr
253          115          120          125
255 Trp Ser Val Arg Gln Ser Lys Arg Pro Thr Gly Ser Asn Ala Thr Ile
256          130          135          140
258 Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser His Gly Met Asn Leu
259 145          150          155          160
261 Gly Ser Asn Trp Ala Tyr Gln Val Met Ala Thr Glu Gly Tyr Gln Ser
262          165          170          175
264 Ser Gly Ser Ser Asn Val Thr Val Trp
265          180          185
267 <210> SEQ ID NO: 6
269 <211> LENGTH: 211
271 <212> TYPE: PRT
273 <213> ORGANISM: Clostridium acetobutylicum
277 <400> SEQUENCE: 6
279 Ser Ala Phe Asn Thr Gln Ala Ala Pro Lys Thr Ile Thr Ser Asn Glu
280 1          5          10          15
282 Ile Gly Val Asn Gly Gly Tyr Asp Tyr Glu Leu Trp Lys Asp Tyr Gly
283          20          25          30
285 Asn Thr Ser Met Thr Leu Lys Asn Gly Gly Ala Phe Ser Cys Gln Trp
286          35          40          45
288 Ser Asn Ile Gly Asn Ala Leu Phe Arg Lys Gly Lys Lys Phe Asn Asp
289          50          55          60
291 Thr Gln Thr Tyr Lys Gln Leu Gly Asn Ile Ser Val Asn Tyr Asn Cys
292 65          70          75          80
294 Asn Tyr Gln Pro Tyr Gly Asn Ser Tyr Leu Cys Val Tyr Gly Trp Thr
295          85          90          95
297 Ser Ser Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp Gly Ser Trp
298          100          105          110
300 Arg Pro Pro Gly Gly Thr Ser Lys Gly Thr Ile Thr Val Asp Gly Gly
301          115          120          125
303 Ile Tyr Asp Ile Tyr Glu Thr Thr Arg Ile Asn Gln Pro Ser Ile Gln
304          130          135          140
307 Gly Asn Thr Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg Thr Lys Arg
308 145          150          155          160
310 Thr Ser Gly Thr Ile Ser Val Ser Lys His Phe Ala Ala Trp Glu Ser
311          165          170          175
313 Lys Gly Met Pro Leu Gly Lys Met His Glu Thr Ala Phe Asn Ile Glu
314          180          185          190
316 Gly Tyr Gln Ser Ser Gly Lys Ala Asp Val Asn Ser Met Ser Ile Asn
317          195          200          205
319 Ile Gly Lys
320          210
322 <210> SEQ ID NO: 7
324 <211> LENGTH: 206
326 <212> TYPE: PRT

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Input Set : A:\PTO.DC.TXT

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328 <213> ORGANISM: Clostridium stercorarium

332 <400> SEQUENCE: 7

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334 Gly Arg Ile Ile Tyr Asp Asn Glu Thr Gly Thr His Gly Gly Tyr Asp
335 1 5 10 15
338 Tyr Glu Leu Trp Lys Asp Tyr Gly Asn Thr Ile Met Glu Leu Asn Asp
339 20 25 30
341 Gly Gly Thr Phe Ser Cys Gln Trp Ser Asn Ile Gly Asn Ala Leu Phe
342 35 40 45
345 Arg Lys Gly Arg Lys Phe Asn Ser Asp Lys Thr Tyr Gln Glu Leu Gly
346 50 55 60
349 Asp Ile Val Val Glu Tyr Gly Cys Asp Tyr Asn Pro Asn Gly Asn Ser
350 65 70 75 80
352 Tyr Leu Cys Val Tyr Gly Trp Thr Arg Asn Phe Leu Val Glu Tyr Tyr
353 85 90 95
355 Ile Val Glu Ser Trp Gly Ser Trp Arg Pro Pro Gly Ala Thr Pro Lys
356 100 105 110
358 Gly Thr Ile Thr Gln Trp Met Ala Gly Thr Tyr Glu Ile Tyr Glu Thr
359 115 120 125
361 Thr Arg Val Asn Gln Pro Ser Ile Asp Gly Thr Ala Thr Phe Gln Gln
362 130 135 140
364 Tyr Trp Ser Val Arg Thr Ser Lys Arg Thr Ser Gly Thr Ile Ser Val
365 145 150 155 160
367 Thr Glu His Phe Lys Gln Trp Glu Arg Met Gly Met Arg Met Gly Lys
368 165 170 175
370 Met Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Tyr
371 180 185 190
373 Ala Asn Val Tyr Lys Asn Glu Ile Arg Ile Gly Ala Asn Pro
374 195 200 205

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376 <210> SEQ ID NO: 8

378 <211> LENGTH: 211

380 <212> TYPE: PRT

382 <213> ORGANISM: Ruminococcus flavefaciens

386 <400> SEQUENCE: 8

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391 Glu Met Trp Asn Gln Asn Gly Gln Gly Gln Ala Ser Met Asn Pro Gly
392 20 25 30
394 Ala Gly Ser Phe Thr Cys Ser Trp Ser Asn Ile Glu Asn Phe Leu Ala
395 35 40 45
397 Arg Met Gly Lys Asn Tyr Asp Ser Gln Lys Lys Asn Tyr Lys Ala Phe
398 50 55 60
400 Gly Asn Ile Val Leu Thr Tyr Asp Val Glu Tyr Thr Pro Arg Gly Asn
401 65 70 75 80
403 Ser Tyr Met Cys Val Tyr Gly Trp Thr Arg Asn Pro Leu Met Glu Tyr
404 85 90 95
407 Tyr Ile Val Glu Gly Trp Gly Asp Trp Arg Pro Pro Gly Asn Asp Gly
408 100 105 110
410 Glu Val Lys Gly Thr Val Ser Ala Asn Gly Asn Thr Tyr Asp Ile Arg
411 115 120 125

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VERIFICATION SUMMARY

DATE: 05/22/2002

PATENT APPLICATION: US/09/990,874

TIME: 12:21:04

Input Set : A:\PTO.DC.TXT

Output Set: N:\CRF3\05222002\I990874.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/990874

CRF Processing Date: 5/22/02 #7
 Edited by: DC
 Verified by: DC (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☒ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95